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Author(s): Arthur, Jennifer Ann

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Genetic algorithm for nuclear data evaluation

Jennifer Arthur

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Initial population

- Normally sample σ_I , $\bar{\nu}_S$, and σ_S using uncertainties around the mean N times
 - σ_I is the induced fission multiplicity distribution width
 - $\bar{\nu}_S$ is the spontaneous fission mean
 - σ_S is the spontaneous fission width

- $$\mathbf{P} = \begin{bmatrix} \sigma_{I1}, \bar{\nu}_{S1}, \sigma_{S1} \\ \sigma_{I2}, \bar{\nu}_{S2}, \sigma_{S2} \\ \dots \\ \sigma_{IN}, \bar{\nu}_{SN}, \sigma_{SN} \end{bmatrix}$$

- Each row of P is a member in the population
 - There are N members total in the population

Fitness (outer loop)

- Ideal is fitness=0
- $FF = \sum \left| \frac{C-E}{E} \right|_{m_1} + \sum \left| \frac{C-E}{E} \right|_{m_2}$, summed over all configurations of all experiments
- Each member of the population has a value of FF (fitness function) assigned to it
- Convergence criteria is that min(FF), which is associated with the most fit member of the population, stops changing more than a certain amount (i.e., 1%)
 - This means that the fittest member of the population is not getting much more fit from generation to generation

Calculate fitness

- Input original (C-E)/E values and original nuclear data values
- Also input sensitivities such as: $\frac{d\left(\frac{C-E}{E}\right)_{m_1}}{d\bar{\nu}_S}$
 - These sensitivities are each specific to a single configuration of a single experiment

Selection (1st part of inner loop)

- N times, pick 2 parents and have them reproduce
 - This creates the next generation of N members
 - There is no limit to how many times a single member can be a parent
- Pick random # between min(FF) and max(FF)
 - I.e., the # can be anywhere from the FF value of the most fit member of the population to the FF value of the least fit member of the population
- 1st 2 members that have $FF \leq \text{random \#}$ are the parents
 - After randomizing population vector of course
- This makes it so that more fit members of the population are more likely to be chosen, but even members with the worst fitness still have a chance to reproduce

Reproduction (2nd part of inner loop)

- Crossover with mutation probability
- Reproduce by averaging the σ_I , \bar{v}_S , and σ_S values of each of the parent pairs chosen in the selection step
- Each time an average is taken, there is a 10% chance that a random value is picked instead of the average
 - Random value (“mutated” value) is generated the same way the initial population was generated

Solution

- The optimized solution is the member of the population that has the minimum (best) value of FF at the time of convergence of the minimum value of FF

Algorithm testing and validation

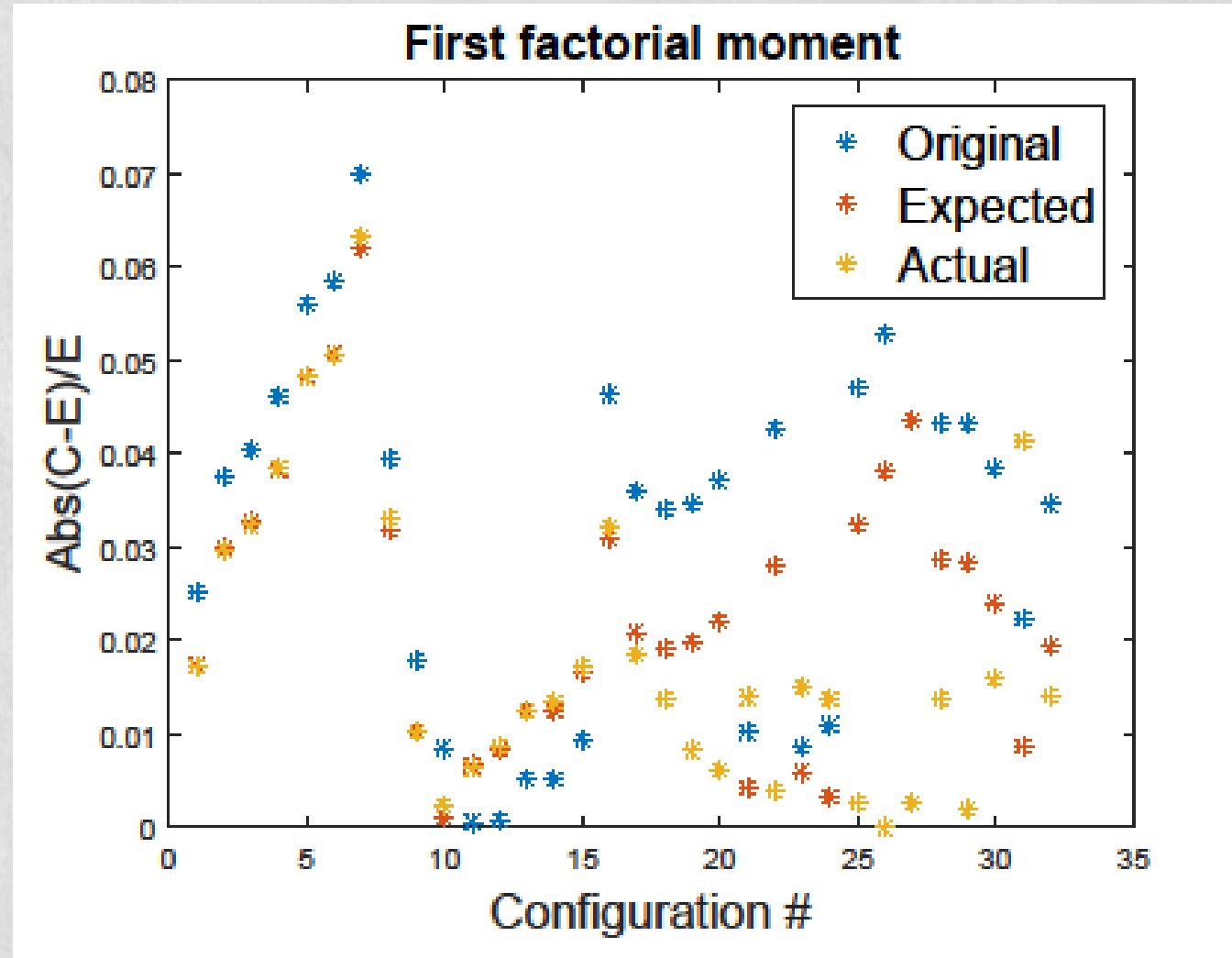
- Using all configurations of BeRP-Ni, BeRP-W, and SCR α P benchmarks
- Original nuclear data:
 - IF width = 1.140
 - SF nubar = 2.151
 - SF width = 1.151
- Optimized nuclear data:
 - IF width = 1.1441
 - SF nubar = 2.1347
 - SF width = 1.1408

Algorithm testing and validation

- Using factorial moments of the Feynman histogram as very basic observables with which to optimize the nuclear data
 - Population size (N) of 1000
 - Mutation rate of 10%
 - Convergence criteria of 0.00001% and a minimum of 100 generations
- Original (C-E)/E values, vs. expected values calculated from sensitivities in algorithm, vs. actual values calculated from MCNP runs

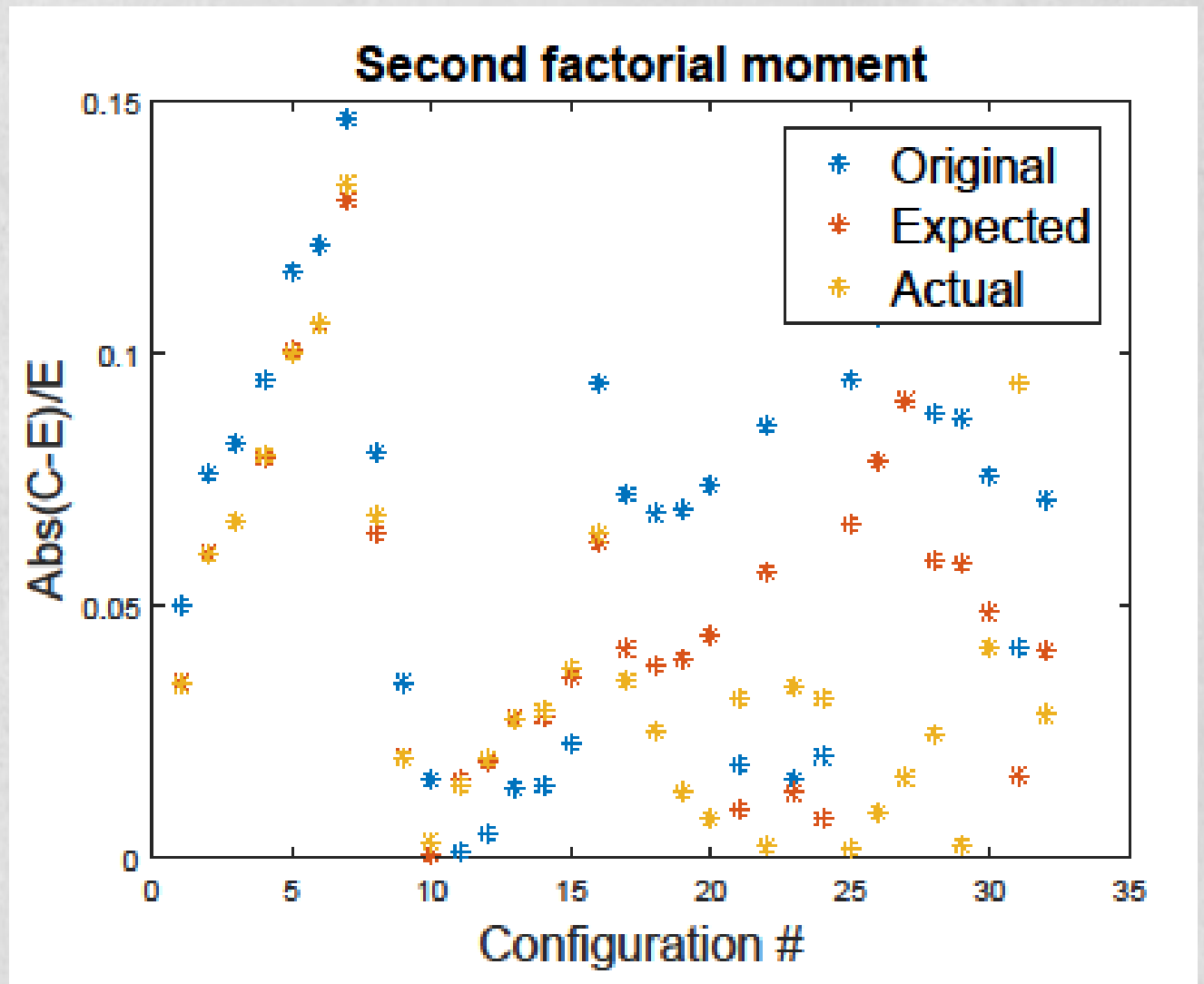
$$m_1 (C-E)/E$$

- Original:
 - 1.0233
- Expected:
 - 0.7585
- Actual:
 - 0.6027



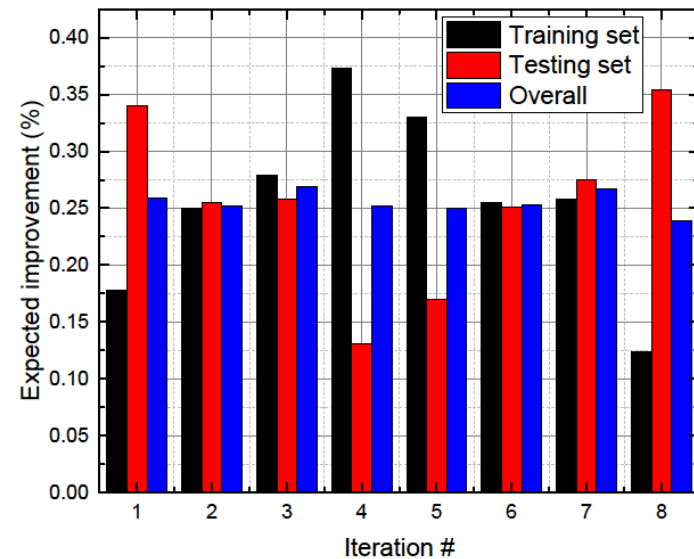
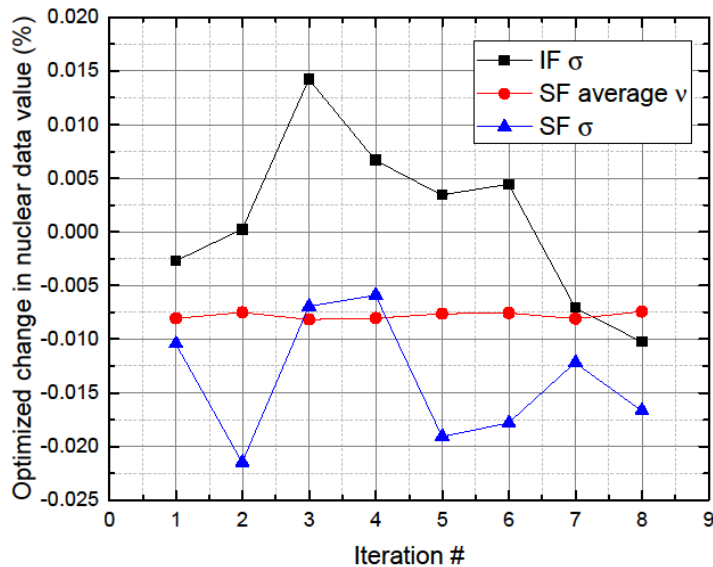
$$m_2 (C-E)/E$$

- Original:
– 2.0762
- Expected:
– 1.5590
- Actual:
– 1.2608



Training and testing data sets

- The 32 configurations were split into 8 different sets of 16 training and 16 testing configurations



Original vs. optimized nuclear data

- Gives 25% expected improvement

Nuclear data	Original	Optimized #1	# Std. dev. change
$\bar{\nu}_S$	2.1510	2.1347	-3.2600
σ_S	1.1510	1.1408	-0.0886
σ_I	1.1400	1.1441	0.0360
Nuclear data	Original	Optimized #2	# Std. dev. change
$\bar{\nu}_S$	2.1510	2.1342	-3.3596
σ_S	1.1510	1.1351	-0.1381
σ_I	1.1400	1.1413	0.0113

Constrained nuclear data

- Less improvement (9% and 17%, compared to previous 25%), but more reasonable changes in nuclear data

Nuclear data	Original	Optimized (1 std. dev. constraint)	# Std. dev. change
\bar{v}_S	2.1510	2.1460	-1.0000
σ_S	1.1510	1.1395	-1.0000
σ_I	1.1400	1.1400	0.0000
Nuclear data	Original	Optimized (2 std. dev. constraint)	# Std. dev. change
\bar{v}_S	2.1510	2.1410	-2.0000
σ_S	1.1510	1.1370	-1.2183
σ_I	1.1400	1.1450	0.4409

Nuclear data optimized to different observables

- 25-27% improvement in all cases

Nuclear data	Original	Optimized for m_1	# Std. dev. change
$\bar{\nu}_S$	2.151	2.1338	-3.4415
σ_S	1.151	1.1399	-0.9675
σ_I	1.14	1.1437	0.3222
Nuclear data	Original	Optimized for m_2	# Std. dev. change
$\bar{\nu}_S$	2.151	2.1333	-3.5468
σ_S	1.151	1.1398	-0.9689
σ_I	1.14	1.1419	0.1638
Nuclear data	Original	Optimized for m_1 and m_2	# Std. dev. change
$\bar{\nu}_S$	2.151	2.1347	-3.26
σ_S	1.151	1.1408	-0.0886
σ_I	1.14	1.1441	0.036

Conclusion

- The genetic algorithm is able to intelligently converge on a set of fission neutron multiplicity distribution parameters that yield improved simulated results
 - Applied to the BeRP-Ni, BeRP-W, and SCR α P subcritical neutron multiplication inference benchmarks
- Does not affect critical benchmark simulations